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☐ 1: AAH09534. PINK1 protein [Ho...[gi:16306928]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAH09534 303 aa linear PRI 18-JUN-2003
DEFINITION PINK1 protein [Homo sapiens].
ACCESSION AAH09534
VERSION AAH09534.1 GI:16306928
DBSOURCE accession BC009534.1
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 303)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnierch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE [22388257](#)

PUBMED [12477932](#)

REFERENCE 2 (residues 1 to 303)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (29-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 14 Row: f Column: 19.

Method: conceptual translation.

FEATURES Location/Qualifiers

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301 aal

//

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PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

☐ 1: BC009534. Homo sapiens PTEN...[gi:16306927] Links

LOCUS BC009534 1553 bp mRNA linear PRI 18-JUN-2003
DEFINITION Homo sapiens PTEN induced putative kinase 1, mRNA (cDNA clone
IMAGE:3891886), partial cds.

ACCESSION BC009534
VERSION BC009534.1 GI:16306927

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1553)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (29-JUN-2001) National Institutes of Health, Mammalian
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USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 14 Row: f Column: 19.

FEATURES

source

Location/Qualifiers

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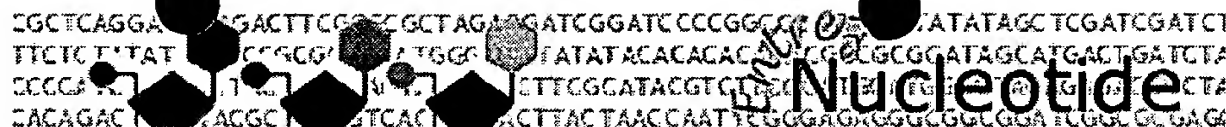
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REFERENCE 8 (bases 1 to 3334)

AUTHORS Riddle,D.L., Swanson,M. and Albert,P.S.
 TITLE Interacting genes in nematode dauer larva formation
 JOURNAL Nature 290 (5808), 668-671 (1981)
 MEDLINE 81173090
 PUBMED 7219552
 COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from C45637.1, AJ131181 and C51447.1.
 On Nov 21, 2002 this sequence version replaced gi:17539551.
 COMPLETENESS: full length.

FEATURES

 source

 Location/Qualifiers

 1..3334

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 /clone_lib="|| [Worm Transcriptome project] The expression profile for the gene, derived from the proportion of animals at each stage in each Kohara library is: Embryo 20%, L1 3%, L2 5%, L3 26%, L4 17%, Adult excluding eggs 29%. || [Predicted cellular localisation] PSORT II analysis, (K. Nakai) trained on yeast data predicts that the subcellular location of this protein is most likely in the nucleus (65%). Less likely possibilities are in the cytoplasm (17%) or in the mitochondria (8%) or in the cytoskeleton (4%) or in the Golgi (4%)."

 gene

 1..3334

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 /locus_tag="4B174"

 /note="affects longevity; insulin like signaling cascade; defective DAuer Formation; synonyms: T07A9.6, CELK00420"

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 /locus_tag="4B174"

 /note="Exon 1 length 237 bp"

 5'UTR

 1..26

 /gene="daf-18"

 /locus_tag="4B174"

 /note="The transpliced leader SL1 (GGTTTAATTACCCAAGTTTGAG visible in yk658f9.3) is present in the mRNA in front of the sequence. There is an in frame stop in the 5'UTR 9 bp before the Met."

 /evidence=experimental

 CDS

 27..2915

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 /locus_tag="4B174"

 /function="Affects longevity"

 /function="Insulin like signaling cascade"

 /function="Defective DAuer Formation"

 /function="[C.elegansII] el375 : defective dauer formation; forms some dauer-like larvae when starved. Partly suppresses Agephenotype of daf-2, age-1. ES1, ME3. NA1. [Larsen et al. 1995; DR]"

 /function="Allele el375"

 /function="El375 : defective dauer formation (daf-7 daf-2 suppressible). ES1 ME3. NA1"

 /note="Eukaryotic regulator of dauer formation and suppressor of age-1 PTEN phosphatidylinositol 3' phosphatase DAF-18, predicted to be nuclear[GB:AF098286] function: suppressor of age-1; phosphatase; [GB:AF126286] function: regulates dauer formation; loss of proteinfunction leads to inability to enter dauer larval stage || [Common ancestor, from TaxBlast with threshold 10-3] Eukaryota || [Closest homologs] Dictyostelium discoideum: gb|AAL99958.1| (score=166); Arabidopsis

thaliana: gb|AL24115.1| (154); Saccharomyces cerevisiae: ref|NP 014271.1| (71); Schizosaccharomyces pombe: ref|NP 596312.1| (96); Caenorhabditis elegans: ref|NP 499926.1| (1912); Drosophila melanogaster: ref|NP 477423.1| (159); Takifugu rubripes: gb|AAL08419.1| (187); Xenopus laevis: gb|AAD46165.1|AF144732 1 (169); Mus musculus: ref|NP 032986.1| (182); Rattus norvegicus: ref|NP 113794.1| (182); Homo sapiens: ref|NP 000305.1| (182)."

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misc feature

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/note="Region: [PSORT] nuclear localization domain: PRKFRYC"

misc feature

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/locus_tag="4B174"

/note="Exon 2 length 245 bp"

misc feature

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/note="Intron length 642 bp, type gt_ag"

exon

483..1348

/gene="daf-18"

/locus_tag="4B174"

/note="Exon 3 length 866 bp"

misc feature

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/locus_tag="4B174"

/note="Intron length 472 bp, type gt_ag"

exon

1349..1951

/gene="daf-18"

/locus_tag="4B174"

/note="Exon 4 length 603 bp"

misc feature

bond(1951,1952)

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/locus_tag="4B174"

/note="Intron length 51 bp, type gt_ag"

exon

1952..2396

/gene="daf-18"

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/note="Exon 5 length 445 bp"

misc feature

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exon

2397..2795

/gene="daf-18"

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